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entry O75807

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[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information


Entry name	O75807_HUMAN
Primary accession number	O75807
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 30, May 2005
Name and origin of the protein	
Protein name	Apoptosis associated protein
Synonym	Protein phosphatase 1, regulatory subunit 15A
Gene name	Name: PPP1R15A
	Synonyms: GADD34
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

References

[1] NUCLEOTIDE SEQUENCE.

DOI=10.1074/jbc.272.21.13731; PubMed=9153226 [NCBI, ExPASy, EBI, Israel, Japan]
Hollander M.C., Zhan Q., Bae I., Fornace A.J. Jr.;
"Mammalian GADD34, an apoptosis- and DNA damage-inducible gene.";
J. Biol. Chem. 272:13731-13737(1997).

[2] NUCLEOTIDE SEQUENCE.

TISSUE=Brain;
DOI=10.1073/pnas.242603899; PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L.
Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., , Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA
sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3] NUCLEOTIDE SEQUENCE.

TISSUE=Brain;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references**Sequence databases**

EMBL U83981; AAC25631.1; -, mRNA. [EMBL / GenBank / DDBJ] [CoDingSequence]
BC003067; AAH03067.1; -, mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases

ModBase O75807.

2D gel databases

SWISS-2DPAGE Get region on 2D PAGE.

Organism-specific gene databases

Ensembl ENSG00000087074; Homo sapiens. [Contig view]

HGNC HGNC:14375; PPP1R15A.

GeneCards PPP1R15A.

GeneLynx PPP1R15A; Homo sapiens.

GenAtlas PPP1R15A.

HOVERGEN [Family / Alignment / Tree]

Gene expression databases

CleanEx HGNC:14375; PPP1R15A.

Ontologies

GO GO:0006915; Biological process: apoptosis (*traceable author statement*).
GO GO:0007050; Biological process: cell cycle arrest (*traceable author statement*).
GO GO:0006974; Biological process: response to DNA damage stimulus (*traceable author statement*).
QuickGo view.

Family and domain databases

ProDom [Domain structure / List of seq. sharing at least 1 domain]

Other

ProtoMap O75807.

PRESAGE O75807.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

None

Features

None

Sequence information

Length: **674** Molecular weight: **73478** CRC64: **B257AA17456D1403** [This is a checksum on the
AA Da sequence]

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MAPGQAPHQA	TPWRDAHPPF	LLSPVMGLLS	RAWSRLRGLG	PLEPWLVEAV	KGAALVEAGL
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
EGEARTPLAI	PHTPWGRRPE	EEAEDSGGPG	EDRETLGLKT	SSSLPEAWGL	LDDDDGMYGE
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
REATSVPRGQ	GSQFADGQRA	PLSPSLIIRT	LQGSCKNPGE	EKAEEEGVAE	EEGVNKFSYP

190 200 210 220 230 240
PSHRECCPAV EEEDDEEAVK KEAHRSTSTA LSPGSKPSTW VSCPGEENQ ATEDKRTERS
250 260 270 280 290 300
KGARKTSVSP RSSGSDPRSW EYRSGEASEE KEEKAHKETG KGEAAPGPQS SAPAQRPLK
310 320 330 340 350 360
SWWCQPSDEE EGEVKALGAA EKDGAEACPP CIPPPSAFLK AWVYWPGEDT EEEEEDEEDE
370 380 390 400 410 420
DSDSGSDEEE GEAEASSSTP ATGVFLKSWV YQPGEDTEEE EDESDTGSA EDEREAETSA
430 440 450 460 470 480
STPPASAFK AWVYRPGEDT EEEDEDEDVS EDKEDDSEAA LGAEESDPHP SHPDQRAHFR
490 500 510 520 530 540
GWGYRPGKET EEEEEAAEDWG EAEPKCFRVA IYVPGEKPPP PWAPPRLPLR LQRRLLKRPET
550 560 570 580 590 600
PTHDPDPETP LKARKVRFSE KVTVHFLAVW AGPAQAARQG PWEQLARDS RFARRITQAQ
610 620 630 640 650 660
EELSPCLTPA ARARAWARLR NPPLAPIPAL TQTLPSSSVS SSPVQTTPLS QAVATPSRSS
670
AAAAAALDLS GRRG

O75807 i
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BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



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MODEL

NPS@

NPSA Sequence analysis
tools



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